

L. Helms

#14

1642

RAW SEQUENCE LISTING DATE: 05/31/2000
PATENT APPLICATION: US/09/250,056B TIME: 13:26:44

Input Set : A:\ESPTO.txt
Output Set: N:\CRF3\05312000\I250056B.raw

5 <110> APPLICANT: Marks, James D
7 Poul, Marie A
11 <120> TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
15 <130> FILE REFERENCE: 2500.116US3 Internalizing ErbB2 Ab
19 <140> CURRENT APPLICATION NUMBER: 09/250,056B
21 <141> CURRENT FILING DATE: 1999-02-12
25 <150> PRIOR APPLICATION NUMBER: 60/082,953
27 <151> PRIOR FILING DATE: 1998-04-24
31 <160> NUMBER OF SEQ ID NOS: 8
35 <170> SOFTWARE: PatentIn Ver. 2.0
39 <210> SEQ ID NO: 1
41 <211> LENGTH: 246
43 <212> TYPE: PRT
45 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
51 <223> OTHER INFORMATION: Description of Artificial Sequence: scFv F5 amino
53 acid sequence
57 <220> FEATURE:
59 <221> NAME/KEY: DOMAIN
61 <222> LOCATION: (31)..(35)
63 <223> OTHER INFORMATION: VH-CDR1
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73 <223> OTHER INFORMATION: VH-CDR2
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83 <223> OTHER INFORMATION: VH-CDR3
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91 <222> LOCATION: (157)..(170)
93 <223> OTHER INFORMATION: VL-CDR1
97 <220> FEATURE:
99 <221> NAME/KEY: DOMAIN
101 <222> LOCATION: (186)..(192)
103 <223> OTHER INFORMATION: VL-CDR2
107 <220> FEATURE:
109 <221> NAME/KEY: DOMAIN
111 <222> LOCATION: (225)..(235)
113 <223> OTHER INFORMATION: VL-CDR3
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119 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
121 1 5 10 15
125 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
127 20 25 30
131 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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133           35           40           45
137 Ser Ala Ile Ser Gly Arg Gly Asp Asn Thr Tyr Tyr Ala Asp Ser Val
139           50           55           60
143 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
145 65           70           75           80
149 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
151           85           90           95
155 Ala Lys Met Thr Ser Asn Ala Phe Ala Phe Asp Tyr Trp Gly Gln Gly
157           100          105          110
161 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
163           115          120          125
167 Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Val
169           130          135          140
173 Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser
175 145          150          155          160
179 Ser Asn Ile Gly Ala Gly Tyr Gly Val His Trp Tyr Gln Gln Leu Pro
181           165          170          175
185 Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Thr Asn Arg Pro Ser
187           180          185          190
191 Gly Val Pro Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser
193           195          200          205
197 Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
199           210          215          220
203 Gln Phe Tyr Asp Ser Ser Leu Ser Gly Trp Val Phe Gly Gly Gly Thr
205 225          230          235          240
209 Lys Leu Thr Val Leu Gly
211           245
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219 <211> LENGTH: 242
221 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: scFv C1 amino
231      acid sequence
235 <220> FEATURE:
237 <221> NAME/KEY: DOMAIN
239 <222> LOCATION: (31)..(35)
241 <223> OTHER INFORMATION: VH-CDR1
245 <220> FEATURE:
247 <221> NAME/KEY: DOMAIN
249 <222> LOCATION: (50)..(66)
251 <223> OTHER INFORMATION: VH-CDR2
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257 <221> NAME/KEY: DOMAIN
259 <222> LOCATION: (99)..(108)
261 <223> OTHER INFORMATION: VH-CDR3
265 <220> FEATURE:
267 <221> NAME/KEY: DOMAIN
269 <222> LOCATION: (157)..(167)

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271 <223> OTHER INFORMATION: VL-CDR1
275 <220> FEATURE:
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279 <222> LOCATION: (184)..(190)
281 <223> OTHER INFORMATION: VL-CDR2
285 <220> FEATURE:
287 <221> NAME/KEY: DOMAIN
289 <222> LOCATION: (223)..(231)
291 <223> OTHER INFORMATION: VL-CDR3
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303 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
305           20           25           30
309 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
311           35           40           45
315 Ser Ser Ile Ser Gly Ser Ser Arg Tyr Ile Tyr Tyr Ala Asp Ser Val
317           50           55           60
321 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
323           65           70           75           80
327 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
329           85           90           95
333 Ala Lys Met Asp Ala Ser Gly Ser Tyr Phe Asn Phe Trp Gly Gln Gly
335           100          105          110
339 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
341           115          120          125
345 Ser Gly Gly Gly Gly Ser Glu Thr Thr Leu Thr Gln Ser Pro Ser Phe
347           130          135          140
351 Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser
353           145          150          155          160
357 Pro Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
359           165          170          175          180
363 Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
365           180          185          190
369 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
371           195          200          205
375 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
377           210          215          220
381 Tyr Asn Ser Tyr Pro Leu Ser Phe Gly Gly Gly Thr Lys Val Glu Ile
383           225          230          235          240
387 Lys Arg
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397 <211> LENGTH: 738
399 <212> TYPE: DNA
401 <213> ORGANISM: Artificial Sequence
405 <220> FEATURE:
407 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleic acid
409     encoding scFv F5 Ab
413 <400> SEQUENCE: 3

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415 cagggtgcagc tgggtggagtc tgggggagggc ttggtacagc ctgggggggtc cctgagactc 60
 417 tcctgtgcag cctctggatt caccctttcgc agctatgccca tgagctgggt cggccaggct 120
 419 ccagggaagg ggctggagtg ggtctcagct attagtggtc gtggtgataa cacatactac 180
 421 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagcgtgtat 240
 423 ctgcaaatga acagcctgag agccgaggac acggccggtt attactgtgc gaaaatgaca 300
 425 agtaacgcgt tcgcatttga ctactggggc cagggaaccc tggtcaccgt ctctcaggt 360
 427 ggaggcggtt caggcggagg tggctctggc ggtggcggat cgcagtctgt gttgacgcag 420
 429 ccgccctcag tgtctggggc ccagggcag agggtcacca tctctgcac tgggagcagc 480
 431 tccaacatcg gggcagggtta tgggtgtacac tgggtaccagc agcttcacag aacagcccc 540
 433 aaactcctca tctatggtaa caccaatcgg ccctcagggg tccctgaccg attctctggc 600
 435 ttcaagtctg gcacctcagc ctccctggcc atcactgggc tccaggctga ggatgaggct 660
 437 gattattact gccagttcta tgacagcagc ctgagtgggt ggggtgttcg cggaggggacc 720
 439 aagctgaccg tgctaggt 738
 443 <210> SEQ ID NO: 4
 445 <211> LENGTH: 726
 447 <212> TYPE: DNA
 449 <213> ORGANISM: Artificial Sequence
 453 <220> FEATURE:
 455 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
 457 encoding scFv C1 amino acid sequence
 461 <220> FEATURE:
 463 <221> NAME/KEY: modified_base
 465 <222> LOCATION: (111)
 467 <223> OTHER INFORMATION: N = A, C, G, OR T
 471 <400> SEQUENCE: 4
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 475 tcctgtgcag cctctggatt caccctttagc agctatgccca tgggctgggt ccgccaggct 120
 477 ccagggaagg ggctggagtg ggtctcatca attagtggca gtatgagata catatattac 180
 479 gcagactccg tgaagggccg gttcaccatc tcccagagaca attccaagaa cagcgtgtat 240
 481 ctgcaaatga acagcctgcg agccgaggac acggccggtt attactgtgc gaaaatggat 300
 483 gcttcgggga gttattttta ttctggggc cagggcaccc tggtcaccgt ctctcaggt 360
 485 ggaggcggtt caggcggagg tggctctggc ggtggcggat cggaaacgac actcacgcag 420
 487 tctccatcct tctgtctgc attttagga gacagaatca ccatcacttg ccgggccagt 480
 489 ccgggcatta ggaattattt agcctgggtat cagcaaaaac cagggaagc ccctaagctc 540
 491 ctgatctatg ctgcatctac ttgcaaaagt ggggtcccat caagggttcag cggcagtgga 600
 493 tctgggacag attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660
 495 tattgtcaac aatataatag ttaccctctc agtttcggcg gagggaccaa ggtggagatc 720
 497 aaacgt 726
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 503 <211> LENGTH: 5
 505 <212> TYPE: PRT
 507 <213> ORGANISM: Artificial Sequence
 511 <220> FEATURE:
 513 <223> OTHER INFORMATION: Description of Artificial Sequence: translocation
 515 sequence
 519 <400> SEQUENCE: 5
 521 Arg Glu Asp Leu Lys
 523 1 5
 529 <210> SEQ ID NO: 6

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Input Set : A:\ESPTO.txt
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531 <211> LENGTH: 4
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535 <213> ORGANISM: Artificial Sequence
539 <220> FEATURE:
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549 Arg Glu Asp Leu
551 1
557 <210> SEQ ID NO: 7
559 <211> LENGTH: 4
561 <212> TYPE: PRT
563 <213> ORGANISM: Artificial Sequence
567 <220> FEATURE:
569 <223> OTHER INFORMATION: Description of Artificial Sequence:: translocation
571 sequence
575 <400> SEQUENCE: 7
577 Arg Asp Glu Leu
579 1
585 <210> SEQ ID NO: 8
587 <211> LENGTH: 4
589 <212> TYPE: PRT
591 <213> ORGANISM: Artificial Sequence
595 <220> FEATURE:
597 <223> OTHER INFORMATION: Description of Artificial Sequence:: translocation
599 sequence
603 <400> SEQUENCE: 8
605 Lys Asp Glu Leu
607 1

VERIFICATION SUMMARY

DATE: 05/31/2000

PATENT APPLICATION: US/09/250,056B

TIME: 13:26:45

Input Set : A:\ESPT0.txt

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